BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

As rescanning documents *will not* correct images, please do not report the images to the Image Problem Mailbox.

Amendments to the Specification

Please add the following subheading on page 1, line 3:

BACKGROUND OF THE INVENTION

Please replace the paragraph on page 1, lines 4-10, with the following rewritten paragraph:

The present invention relates to a new nucleic material of the endogenous retroviral genomic type, various nucleotide fragments comprising it or which are obtained from said material, as well as their use as a marker for at least one autoimmune disease or a pathology which is associated with it, a pathological pregnancy or an unsuccessful pregnancy.

Please add the following subheading on page 3, between lines 33 and 34:

SUMMARY OF THE INVENTION

Please replace the paragraph on page 5, lines 14-21, with the following rewritten paragraph:

This material is also characterized in that its genome comprises a reference nucleotide sequence, encoding any polypeptide exhibiting, for any contiguous sequence of at least 30 amino acids, at least 50% homology, ~~and~~ preferably at least 70% homology, more preferably at least 80% homology, and even more preferably at least 90% homology with a peptide sequence capable of being encoded by at least a functional part of the reference nucleotide sequence as defined above.

Please replace the paragraph on page 10, lines 5-8, with the following rewritten paragraph:

- "functional" is understood to mean the characteristic according to which a nucleotide sequence, a nucleic material or a nucleotide fragment comprises an "~~an~~ informational sequence,";

Please add the following subheading on page 15, between lines 20 and 21:

BRIEF DESCRIPTION OF THE DRAWINGS

Please replace the paragraph on page 16, lines 7-8, with the following rewritten paragraph:

the splice donor sites ~~(~~[DS1 (SEQ ID NOs: 36 and 38) and DS2 (SEQ ID NO: 39)] and acceptor sites ~~(~~[AS1 (SEQ ID NOs: 37 and 40), AS2 (SEQ ID NO: 41) and ~~to~~ AS3 (SEQ ID NO: 42)];

Please replace the paragraph on page 16, line 30 through page 17, line 5, with the following rewritten paragraph:

- Figure 5 represents the alignment of the 5' and 3' flanking regions of the clone RG083M05 [SEQ ID NO: 43 (5-RG-28000-28872) and SEQ ID NO: 44 (3-RG-37500-38314)] with the terminal 5' and/or 3' regions of some placental clones [SEQ ID NO: 45 (3-PH74.2358-2782), SEQ ID NO: 46 (3-C4C5.710-1136), SEQ ID NO: 47 (5-6A2.1-600), SEQ ID NO: 48 (5-PH74.1-530) and SEQ ID NO: 49 (5-24.4.1-486)]; the CAAC tandem flanking the 3' and 5' LTRs is doubly underlined under the DNA sequences, the consensus LTR sequence of 783 bp (base pairs) (SEQ ID NO: 15) is indicated under the alignment; the PPT upstream of the 5' end of LTR and the PBS downstream of the 3' end of LTR are indicated; the U3R and U5 regions are indicated; the sites corresponding to the binding of the transcription factor are underlined and numbered from 1 to 6; the region -73 to 284 corresponds to the sequence evaluated in "CAT assay"; * corresponds to putative sites for "capping"; [polyA] indicates the polyadenylation signal.

Please replace the paragraph on page 17, lines 6-19, with the following rewritten paragraph:

- Figure 6 represents a putative sequence of a HERV-W envelope polypeptide (ORF1) (SEQ ID NO: 33) obtained from 3 different placental cDNA clones; the leader peptide (L),

the surface protein (SU) and the transmembrane protein (TM) are indicated by arrows; the hydrophobic fusion peptide and the transmembrane carboxy region are underlined by a single line and a double line, respectively; the immunosuppression region is indicated in italics; the potential glycosylation sites are indicated by dots; the divergent amino acids are indicated on the bottom line; Figure 6 also presents the open reading frames corresponding to ORF2 (SEQ ID NO: 34) and ORF3 (SEQ ID NO: 35) as described in Figure 2, and more particularly ~~their~~ the homologies of portions thereof (SEQ ID NOs: 50 and 51) with the retroviral regulatory genes (SEQ ID NOs: 52 and 53, respectively).

Please add the following subheading on page 17, between lines 19 and 20:

DETAILED DESCRIPTION OF PREFERRED EMBODIMENTS

Please replace the paragraph on page 19, lines 20-23, with the following rewritten paragraph:

/note="splice junction (splice donor site ATCCAAAGTG-GTGAGTAATA (SEQ ID NO: 36) and splice acceptor site CTTTTTTCAG-ATGGGAAACG (SEQ ID NO: 37) clone RG083M05, GenBank accession AC000064)"

Please replace the paragraph on page 21, line 35 through page 22, line 20, with the following rewritten paragraph:

The reconstructed sequence (RNA) is integrally contained inside the genomic clone RG083M05 (9.6 Kb) and exhibits a 96% similarity with two discontinuous regions of this clone which also contains repeat regions at each end. The alignment of the experimental sequences corresponding to the 5' and 3' regions of the genomic RNA reconstructed with the DNA of the clone RG083M05 [5' (5-RG-28000-28872) (SEQ ID NO: 43) and 3' (3-RG-37500-38314) (SEQ ID NO: 44)] made it possible to deduce an LTR sequence and to identify elements characteristic of the retroviruses, in particular those involved in the reverse transcription, namely PBS downstream of the 5' LTR and the PPT upstream of the

3' LTR (cf Figure 5). It is observed that the U3 element is extremely short in comparison with that observed in the mammalian type C retroviruses, and is comparable in size to the U3 region generally described in the type D retroviruses and the avian retroviruses. The region corresponding to bases 2364 to 2720 of the clone cl.PH74 (SEQ ID NO: 7) was amplified by PCR and subcloned into the vector pCAT3 (Promega) in order to carry out the evaluation of the promoter activity. A significant activity was found in HeLa cells by the so-called "CAT assay" method showing the functionality of the promoter sequence of the LTR.